

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hawkins, Phillip R.
Murry, Lynn E.

(ii) TITLE OF THE INVENTION: HUMAN PHOSPHOLIPASE INHIBITOR

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
- (B) STREET: 3174 Porter Drive
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: U.S.
- (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To Be Assigned
- (B) FILING DATE: Filed Herewith

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Luther, Barbara J.
- (B) REGISTRATION NUMBER: 33,954
- (C) REFERENCE/DOCKET NUMBER: PF-0059-1 US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415-855-0555
- (B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB02
- (B) CLONE: CONSENSUS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

NCAATGGGCC GGCGTGGGA AGGGTGAATG TGGGTCCAGA CCCGCCCCTC CTCAGCTTCC

60

TATAAAAGCT	GGGGACCAAGG	TACTGCTGAT	ACACACACCCA	TGAGGCTCTC	CAGGAGACCA	120
GAGACCTTTC	TGCTGGCCTT	TGTGTTGCTC	TGCACCCCTCC	TGGGCTTGG	GTGCCCACTA	180
CACTGCCAAA	TATGTACGGC	GGCGGGGAGC	AGGTGCCATG	GCCAAATGAA	GACCTGCAGC	240
AGTGACAAGG	ACACATGTGT	GCTCCTGGTC	GGGAAGGCTA	CTTCAAAGGG	CAAGGAGTTG	300
GTGCACACCT	ACAAGGGCTG	CATCAGGTCC	CAGGACTGCT	ACTCCGGCGT	TATATCCACC	360
ACCATGGGCC	CCAAGGACCA	CATGGTAACC	AGCTCCTTCT	GCTGCCAGAG	CGACGGCTGC	420
AACAGTGCCT	TTTTGTCTGT	TCCCTTGACC	AATCTTACTG	AGAATGGCCT	GATGTGCCCC	480
GCCTGCACTG	CGAGCTTCAG	GGACAAATGC	ATGGGGCCCA	TGACCCACTG	TACTGGAAAG	540
GAAAACCACT	GCGTCTCCTT	ATCTGGACAC	GTGCAGGCTG	GTATTTCAA	ACCCAGATT	600
GCTATGCGGG	GCTGTGCTAC	AGAGAGTATG	TGCTTTACCA	AGCCTGGTGC	TGAAGTACCC	660
ACAGGCACCA	ATGTCCTCTT	CCTCCATCAT	ATAGAGTGCA	CTCACTCCCC	CTGAAAAGCT	720
ATCTGAACAG	AGGAAGATAA	TGTAGTGTGA	AGTCCCCATT	TGTCCTCAGC	CTGTAACCTC	780
CCCGTGTGCC	TATAAAAGAAG	TTAATAGAGC	AAAAAAAAAA	AAAAAAAAAA	AAACTCGAG	839

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) IMMEDIATE SOURCE:
 (A) LIBRARY: THP1LPB02
 (B) CLONE: CONSENSUS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: GI 501050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Tyr Leu His Thr Ile Cys Leu Leu Phe Ile Phe Val Ala Arg
1 5 10 15
Gly Asn Ser Arg Ser Cys Asp Phe Cys His Asn Ile Gly Lys Asp Cys
20 25 30
Asp Gly Tyr Glu Glu Glu Cys Ser Ser Pro Glu Asp Val Cys Gly Lys
35 40 45
Val Leu Leu Glu Ile Ser Ser Ala Ser Leu Ser Val Arg Thr Val His
50 55 60
Lys Asn Cys Phe Ser Ser Ser Ile Cys Lys Leu Gly Gln Phe Asp Val
65 70 75 80
Asn Ile Gly His His Ser Tyr Ile Arg Gly Arg Ile Asn Cys Cys Glu
85 90 95
Lys Glu Leu Cys Glu Asp Gln Pro Phe Pro Gly Leu Pro Leu Ser Lys
100 105 110
Pro Asn Gly Tyr Tyr Cys Pro Gly Ala Ile Gly Leu Phe Thr Lys Asp
115 120 125
Ser Thr Glu Tyr Glu Ala Ile Cys Lys Gly Thr Glu Thr Lys Cys Ile
130 135 140
Asn Ile Val Gly His Arg Tyr Glu Gln Phe Pro Gly Asp Ile Ser Tyr
145 150 155 160
Asn Leu Lys Gly Cys Val Ser Ser Cys Pro Leu Leu Ser Leu Ser Asn
165 170 175
Ala Thr Phe Glu Gln Asn Arg Asn Tyr Leu Glu Lys Val Glu Cys Lys
180 185 190
Asp Ala Ile Arg Leu Ala Ser Leu
195 200

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

PF-0059-5 CON

- (A) LIBRARY: HMC1N0T01
(B) CLONE: 8941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAGGCCTAG	GGTTAGGCAA	GACCTTGAGG	CAGGGGTTGA	AGCCAGGGAG	TGGTCAGCCA	60
GCACGTCCC	TGCCGTCCC	CATCCCACAG	AGGGCAAGGA	GTTGGTGCAC	ACCTACAAGG	120
GCTGCATCAG	GTCCCAGGAC	TGCTACTCCG	GCGTTATATC	NACCACCATG	GGCCCCAAGG	180
ACCACATGGT	AACCAGCTCC	TTCTGNTGCC	AGAGCGACGG	CTGCAACAGT	GCCTTTTGT	240
CTGTTCCCTT	GACCAATCTT	ACTGAGAAATG	GCCTGATGTG	CCCNNGCTGCA	CTGCGAGTTT	300
NAGGGNCAAA	ATNCATGGGG	GCCCATT				327

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1LPB01
(B) CLONE: 10033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTGCTCTNC	ACCCCTCCTGG	GTCTTGGGTG	CCCAC TACAC	TGCGAAATAT	GTACGGCGGC	60
GGGGAGCAGG	TGCCATGGCC	AAATGAAGAC	CTGCAGCAGT	GACAAGGACA	CATGTGTGCT	120
CCTGGTGGGG	AAGGCTACTT	CAAAGGGCAA	GGAGTTGGTG	CACACCTACA	AGGGCTGCAT	180
CAGGTCCCAG	GACTGCTACT	CCGGCGTTAT	ATCCACCACC	ATGGGGCCCCA	AGGACCACAT	240
GGTAACCAGC	TCCTTCTGCT	GCAGAGCGAC	GGCTGCAACA	GTGCCTTTT	GTCTGTTCCC	300
TTGACCAATC	TTACTGAGAA	TGGT				324

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1LPB01
(B) CLONE: 10644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACACATGTG	TNCTCCTGGT	CGGGAAGGCT	ACTTCAAAGG	GCAAGGAGTT	GGTGCACACC	60
TACAAGGGCT	GCATCAGGTN	CCAGGACTGC	TACTCCGGNG	TTATATCCAC	CACCATGGGC	120
CCCAAGGACC	ACATGGTAAC	CAGCTCCTTC	TGCTGCCAGA	GCGACGGCTG	CAACAGTGCC	180

PF-0059-5 CON

TTTTTGTCTG TTCCCTTGAC CAATNTTACT GAGAATNGNC TGATGTGCC CGNCTGCACT	240
GNGAGCTTCA GGGACAAATG CT	262

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB01
- (B) CLONE: 10774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACACATGTG TGCTCCTGGT CGGGAAGGCT ACTTCAAAGG GCAAGGAGTT GGTGCACACC	60
TACAAGGGCT GCATCAGGTC CCAGGACTGC TACTCCGGNG TTATATCCAC CACCATGGGC	120
CCCAAGGACC ACATGGTAAC CAGCTCCCTTC TGCTGCCAGA GCGACGGCTG CAAACAGTGCC	180
TTTTTGTCTG TTCCCTTANC CAATCTTACT GAGAATGGCC TGATGTGCC CGNCTGAACT	240
NCGAGCTTCA GGGACAAATN CATGGGNNA TGACCCACTG TACTGGNAAG NNAAACCACT	300
GNGTGTCCCTT	310

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PEB01
- (B) CLONE: 71854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCCGGCGTT ATATCCACCA CCATGGGCC CAAGGACAC ATGGTAACCA GCTCCTTCTG	60
CTGCCAGAGC GACGGCTGCA ACANTGCCTT TTTNTNTGTT CCCTTGACCA ATCTTACTGA	120
GAATGGCCTG ATGTGCCCG CCTGCACTGC GAGCTTCAGG GACAAATGCA TGGGGCCCCAT	180
GACCC	185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

PF-0059-5 CON

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PEB01
- (B) CLONE: 72861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTGGTGCAC ACCTACAAGG GCTGCATCAG GTCCCAGGAC TTCTACTCCG GNNTTATATC	60
CACCACCATG GGCCCCAAGG ACCACATGGT AACCAAGCTCC TTNTGCTGCC AGAGCGACGG	120
CTGCAACATT GCCTTTTNT NTGTNCCCTT G	151

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PEB01
- (B) CLONE: 74452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGACTGCT ACTCCGGNGT TATATCCACC ACCATGGGCC CCAAGGACCA CATGGTAACC	60
AGCTCCTTCT GCTGCCAGAG CNACGGCTGC AACANTGCCT TTNTGTCTGT NCCCTTGACC	120
AATCTNACTG AGAATNGCCT GATT	144

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB02
- (B) CLONE: 155045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CNTGGCCTTA GTTTTNCNCT CACCCTCCNG GGTCTNGGT GCCCACNACA CTGCGAANTA	60
TGTACGGCGG CGGGTAGCAG GTTCCATGNC CAAATNAAGA NCTTCANCNG TGACAAGGAC	120
ACATGTNTGC TCCTGGTCGG NAAGNCTACT TCAAAGGGCA AGGAGTTGGT GCAC	174

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB02
- (B) CLONE: 156817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGGCCTTTG	TGTTGCTCTG	CACCCTCCTG	GGTCTTGGGT	GCCCAC TACA	CTGCGAAATA	60
TGTACGGCGG	CGGGGAGCAG	GTGCCATGGC	CAAATGAAGA	CCTGCAGCAG	TGACAAGGAC	120
ACATGTGTGC	TCCTGGTCGG	GAAGGCTACT	TCAAAGGGCA	AGGAGTTNGT	GCACACCTAC	180
AAGGGCTGCA	TCAT					194

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PGANNOT01
- (B) CLONE: 619856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAAGAGAC	CATNCCAGGA	AGTTGTGGGG	TTGGGGAGGC	CTAGGGTTAG	GCAAGACCTT	60
GAGGCAGGGG	TTGAAGCCAG	GGAGTGGTCA	GCCAGCACTG	TCCCTGCCTG	TCCCCATCCC	120
ACAGAGGGCA	AGGAGTTGGT	GCACA ACTAC	AAGGGCTGCA	TCAGGTCCCA	GGACTGCTAC	180
TNCGGNGTTA	TATCCACCA C	CATGGGCC	CCC AAGGACCACA	TGGT		224

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSN0T02

PF-0059-5 CON

(B) CLONE: 683480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTGGTGCAC	ACCTACAAGG	GCTGCATCAG	GTCCCAGGAC	TGCTACTCCG	GCGTTATATN	60
CACCACCATG	GGNCCCAAGG	ACCACATGGT	AACCAGCTCC	TTNTGCTGCC	AGAGCGACGN	120
CTGCAACAGT	GCCTTTTGT	CTGTTCCCTT	GACCAATCTT	ACTGAGAATG	GCCTGATGTG	180
CCCCGNCTGC	ACTGCGAGCT	TNAGGGACAA	ATGCATGGGG	CCCATGACCC	ACTGTACTGG	240
AGAGGAAAAC	CA					252

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT11
- (B) CLONE: 1291208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

GGGAATCCA	GTTCTTGCAG	CCACTGGGAA	TCAAGAGGCC	CAAATCCGTC	TTGGTCTTNN	60
NNNNNNNNNN	NNNNNNNCAA	TGGGCCGGCC	GTGGGAAGGG	TGAATGTGGG	TCCAGACCCG	120
CCCCTCCTCA	GCTTCCTATA	AAAGCTGGGG	ACCAGGTACT	GCTGATACAC	ACACCATGAG	180
GCTCTCCAGG	AGACCAGAGA	CCTTTCTGCT	GGCCTTTGTG	TTGCTCTGCA	CCCTCCTGGG	240
TCTTGGGTGC						250